

A New Species of *Hemiphyllodactylus* Bleeker, 1860 (Reptilia: Squamata) from Hunan Province, China

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Abstract A new species of gekkonid, *Hemiphyllodactylus dupanglingensis* **sp. nov.**, is described based on six specimens from Hunan Province, China. The new species is phylogenetically close to *H. zugi*, *H. hongkongensis*, *H. dushanensis*, and *H. huishuiensis*, and can be distinguished from its congeners by the following combination of characters: 9–11 chin scales; postmental scales enlarged; 9–12 infralabials, 11–14 supralabials; 14–16 dorsal scales and 10–11 ventral scales longitudinally arranged at the midbody contained with one eye diameter; a manual lamellar formula of 4–4–5–4 or 4–5–5–4 and a pedal lamellar formula of 4–5–5–5 or 5–6–6–4; 21–25 continuous precloacal and femoral pores in males.

Keywords *Hemiphyllodactylus dupanglingensis* **sp. nov.**, molecular phylogeny, morphology, slender gecko, taxonomy

1. Introduction

The genus *Hemiphyllodactylus* Bleeker, 1860 consists of 35 species of small geckos distributed in South and Southeast Asia and the Indo-Pacific region (Zug, 2010; Agarwal *et al.*, 2019; Eliades *et al.*, 2019). Morphological similarity makes species identification difficult. Before 2013, only nine species and three subspecies had been recognized mainly based on morphological characters: *H. typus* Bleeker, 1860, *H. aurantiacus* Beddome, 1870, *H. larutensis* Boulenger, 1900, *H. harteri* Werner, 1900, *H. yunnanensis* Boulenger, 1903, *H. insularis* Taylor, 1918, *H. margarethae* Brongersma, 1931, *H. ganoklonis* Zug, 2010, and *H. titiwangsaensis* Zug, 2010, and three subspecies *H. yunnanensis dushanensis* Zhou and Liu, 1981, *H. y. jinpingensis* Zhou and Liu, 1981, and *H. y. longlingensis* Zhou and Liu, 1981. Integrative taxonomy, using both molecular phylogenetic and morphological analyses (Grismer *et al.*, 2013), has revealed a high level of species diversity. The subspecies *H. y. dushanensis*, *H. y. jinpingensis*, and *H. y. longlingensis* have been raised to full species status, and occurrences of at least nine possibly undescribed species in Indochina and Southeast Asian Islands were suggested. Agarwal *et al.* (2019) reported three additional undescribed clades in this genus from peninsular India in South Asia.

Most species of *Hemiphyllodactylus* are small and nocturnal with cryptic body coloration and low population density. As such, researchers seldom encounter them in the field (Zug, 2010; Grismer *et al.*, 2013; Agarwal *et al.*, 2019; Eliades *et al.*, 2019). During the wild terrestrial vertebrate surveys in Dupangling, Dao

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County, Hunan Province, China, in 1998, three specimens of *Hemiphyllodactylus* from Kongshuyan in Dupangling were accidentally collected. After a preliminary morphological description, these specimens were tentatively assigned to the species *H. yunnanensis* (Deng *et al.*, 1998). *H. yunnanensis* is widely distributed ranging through China, Myanmar, Thailand, Laos, and Vietnam (Zug, 2010). Some species of *Hemiphyllodactylus*, once considered as *H. yunnanensis*, have now been described as new species by using an integrative taxonomic approach. This genus has high species diversity, localized population distribution, and little movement between populations. Due to its isolation of other collection localities, the taxonomic status of the Dupangling population from Hunan Province was reconsidered. However, we could not obtain access to the preserved material of the three specimens and were uncertain of their taxonomic status. During herpetological surveys in Dupangling, Hunan Province, from 2018 to 2019, we made six collections of *Hemiphyllodactylus* in the same locality reported by Deng *et al.* (1998). Based on close examination, comparison with its congeners, and a phylogenetic analysis, we determined that the geckos from Dupangling are an undescribed species. The phylogeny results show that the population of *Hemiphyllodactylus* from Dupangling is a sister group of *H. zugi*, *H. hongkongensis*, *H. dushanensis*, and *H. huishuiensis*.

2. Materials and Methods

2.1. Phylogenetic Analysis Genomic DNA was extracted from 95% ethanol-preserved liver tissues, by using a TSINGKE (<https://www.tsingke.net>) DNA extraction kit. The mitochondrial ND2 (NADH dehydrogenase subunit 2) gene from three samples was amplified by PCR using primer pairs ND2f101A (5'-CAACAGAAGCCACAACAAAAT-3') (modified from ND2f101; Nguyen *et al.* 2013) and HemiR (5'-GAAGAAGAGGCTTGKAGGCT-3') (Nguyen *et al.*, 2013). The amplifications program followed the sequence of 98°C for 2 min; 35 cycles of 98°C for 10 s, 55°C for 10 s, 72°C for 10 s; and a final extending step at 72°C for 2 min. PCR purification and sequencing were performed by Beijing Tsingke Biological Technology Co. Ltd. We downloaded sequences of the orthologous gene of *Hemiphyllodactylus* and an outgroup available from GenBank, following the recent phylogenetic and taxonomic studies of *Hemiphyllodactylus* (Grismer *et al.*, 2017; Sukprasert *et al.*, 2018; Sung *et al.*, 2018; Agarwal *et al.*, 2019; Eliades *et al.*, 2019) (Table S1). DNA sequences were aligned by the Clustal W algorithm with default

parameters (Thompson *et al.*, 1997) and trimmed with gaps partially deleted in MEGA 6 (Tamura *et al.*, 2013). The partitions were tested in jmodeltest v2.1.2 with Akaike and Bayesian information criteria, all resulting in the best-fitting nucleotide substitution models of GTR+I+G. Sequenced data were analyzed using Bayesian inference (BI) in MrBayes 3.2.4 (Ronquist *et al.*, 2012), and maximum likelihood (ML) in RaxmlGUI 1.3 (Silvestro and Michalak, 2012). Two independent runs were conducted in a BI analysis, each of which was performed for 10 000 000 generations and sampled every 1000 generations with the first 25% samples discarded as burn-in, resulting in a potential scale reduction factor (PSRF) of < 0.005. In ML analysis, the bootstrap consensus tree inferred from 1000 replicates was utilized to represent the evolutionary history of the taxa analyzed. Genetic distances between and within species were calculated in MEGA 6 using the uncorrected *p*-distance model base on ND2 gene.

2.2. Morphological Analysis Measurements were taken for the specimens from Dupangling by a digital caliper (0.01 mm, nearest to 0.1 mm), and meristic traits were counted under a binocular scope (Leica Z16 APO/DFC550) (Table 1). High-quality images of the holotype were taken with a Leica Z16 APO/DFC550. The mensural and meristic characters and abbreviations followed Zug (2010), Grismer *et al.* (2013) and Grismer *et al.* (2018). These were eye diameter (EyeD), the maximum horizontal diameter of the exposed eyeball; head length (HeadL), the distance from the posterior margin of the retroarticular process of the lower jaw to the tip of the snout; head width (HeadW), measured at the angle of the jaws; nares-eye length (NarEye), measured from the anterior margin of the eyeball to the posterior margin of the external nares; snout-eye length (SnEye), measured from the anteriormost margin of the eyeball to the tip of snout; internarial width (SnW), measured between the nares across the rostrum; snout-vent length (SVL), taken from the tip of snout to the vent; tail length (TailL), taken from the vent to the tip of the tail, original or regenerated; and trunk length (TrunkL), taken from the posterior margin of the forelimb at its insertion point on the body to the anterior margin of the hindlimb at its insertion point on the body. The meristic characters included chin scales (Chin), the number of scales touching internal edge of infralabials and mental from juncture of 2nd and 3rd infralabials on left and right; circumnasal scales (CircNa), the number of scales contacting the nares; scales between nasals (SnS), the number of scales touching rostral scale between left and right supranasals; dorsal scales (Dorsal), the number of scales longitudinally at midbody on dorsum contained

Table 1 Measurements and scale counts of *Hemiphyllodactylus dupanglingensis* sp. nov.

Spec No.	CSUFT 00401	CSUFT 00402	CSUFT 00403	CSUFT 00404	CSUFT 00405	CSUFT 00406
Sex	F	M	M	M	M	M
Chin	10	10	9	11	11	11
Postmentals distinctly enlarged (1) or not (0)	1	1	1	1	1	1
CircNa	4	3	4	3	3	3
SnS	2	2	2	2	3	3
Suplab	11	11	11	12	11	14
Inflab	12	9	9	10	10	9
Dorsal	15	15	16	15	14	14
Ventral	11	11	10	10	11	11
2–5FingLm	4–5–5–4	4–4–5–4	4–4–5–4	4–4–5–4	4–4–5–4	/
2–5ToeLm	4–5–5–5	4–5–5–5	4–5–5–5	5–6–6–4	4–5–5–5	/
1FingLm	5	4	5	5	5	/
1ToeLm	5	4	4	5	5	/
Precloacal and femoral pore series separate (1) or continuous (0)	0	0	0	0	0	0
Pore	0	24	25	21	25	21
CloacS	1	1	2	2	1	2
EyeD	2.5	2.6	2.5	2.7	2.5	2.7
HeadL	9.8	11.2	10.3	11.1	10.5	10.9
HeadW	7.5	7.5	7.2	7.6	6.8	7.8
NarEye	3.3	3.2	3.0	3.1	3.2	3.3
SnEye	4.5	4.7	4.2	4.3	4.3	4.6
SnW	1.8	1.5	1.4	1.6	1.7	1.7
TailL	\	29.3	32.5	\	37.9	40.1
HeadD	4.0	4.5	4.6	4.6	4.2	4.5
SVL	40.8	41.0	39.5	40.8	39.4	44.7
TrunkL	18.7	19.4	17.2	19.7	18.1	22.8
TrunkL/SVL	0.46	0.47	0.44	0.48	0.46	0.51
HeadL/SVL	0.24	0.27	0.26	0.27	0.27	0.24
HeadW/SVL	0.18	0.18	0.18	0.19	0.17	0.17
HeadW/HeadL	0.77	0.67	0.7	0.68	0.65	0.72
SnEye/HeadL	0.46	0.42	0.41	0.39	0.41	0.42
NarEye/HeadL	0.34	0.29	0.29	0.28	0.3	0.3
EyeD/HeadL	0.26	0.23	0.24	0.24	0.24	0.25
SnW/HeadL	0.18	0.13	0.14	0.14	0.16	0.16
EyeD/NarEye	0.76	0.81	0.83	0.87	0.78	0.82
SnW/HeadW	0.24	0.2	0.19	0.21	0.25	0.22

Note: / in CSUFT 00406 line indicates features that could not be identified because the specimen was poorly preserved.

within one EyeD; ventral scales (Ventral), the number of scales longitudinally at midbody on ventral contained with one EyeD; infralabial scales (Inflab) and supralabial scales (Suplab), the number of enlarged scales from rostral to top of mouth curve, usually equivalent to end of orbit; femoral and precloacal pores series (Pore), the total number of precloacal and femoral pores in males; the number of subdigital lamellae wider than long on the first finger (1FingLm) and toe (1ToeLm); lamellar formula, determined as the number of U-shaped subdigital lamellae

on the digital pads on digits 2–5 of the hands (2–5FingLm) and feet (2–5ToeLm); and the number of cloacal spurs (CloacS). The coloration characters include the presence /absence of dark pigmentation in the gonadal tracts and caecum; a dark postorbital stripe extending to at least the neck; and a linear series of white postorbital or trunk spots, light-colored anteriorly projecting arms of the postsacral marking.

We examined morphological characters of the specimens from Dupangling and compared them with

those of the known species of *Hemiphyllodactylus* based on relevant literature including *H. arakuensis* (Agarwal *et al.*, 2019), *H. aurantiacus* (Zug, 2010; Agarwal *et al.*, 2019), *H. banaensis* (Ngo *et al.*, 2014), *H. bintik* (Grismer *et al.*, 2015), *H. changningensis* (Guo *et al.*, 2015), *H. chiangmaiensis* (Grismer *et al.*, 2014b), *H. cicak* (Cobos *et al.*, 2016), *H. dushanensis* (Zhou *et al.*, 1981; Grismer *et al.*, 2013), *H. engganoensis* (Grismer *et al.*, 2014a), *H. flaviventris* (Sukprasert *et al.*, 2018), *H. ganoklonis* (Zug, 2010), *H. harterti* (Zug, 2010; Grismer *et al.*, 2013), *H. hongkongensis* (Sung *et al.*, 2018), *H. huishuiensis* (Yan *et al.*, 2016), *H. indosobrinus* (Eliades *et al.*, 2019), *H. insularis* (Zug, 2010; Grismer *et al.*, 2013), *H. jinpingensis* (Zhou *et al.*, 1981; Grismer *et al.*, 2013), *H. jnana* (Agarwal *et al.*, 2019), *H. khlonglanensis* (Sukprasert *et al.*, 2018), *H. kiziriani* (Nguyen *et al.*, 2014), *H. kolliensis* (Agarwal *et al.*, 2019), *H. larutensis* (Zug, 2010; Grismer *et al.*, 2013), *H. linnwayensis* (Grismer *et al.*, 2017), *H. longlingensis* (Zhou *et al.*, 1981; Grismer *et al.*, 2013), *H. margarethae* (Zug, 2010; Grismer *et al.*, 2013), *H. montawaensis* (Grismer *et al.*, 2017), *H. serpispecus* (Eliades *et al.*, 2019), *H. tehtarik* (Zug, 2010; Grismer *et al.*, 2013), *H. titiwangsaensis* (Zug, 2010; Grismer *et al.*, 2013), *H. tonywhitteni* (Grismer *et al.*, 2017), *H. typus* (Zug, 2010; Grismer *et al.*, 2013), *H. uga* (Grismer *et al.*, 2018), *H. yunnanensis* (Zhou *et al.*, 1981; Grismer *et al.*, 2013), *H. ywanganensis* (Grismer *et al.*, 2018), and *H. zugii* (Nguyen *et al.*, 2013).

3. Results

Phylogenetic analyses. The ML and BI phylogenetic trees were constructed based on DNA sequences of the mitochondrial ND2 gene with a total length of 670 bp. The two analyses resulted in identical topologies, suggesting that the population of *Hemiphyllodactylus* from Dupangling is sister to a clade comprising *H. zugii*, *H. hongkongensis*, *H. dushanensis*, and *H. huishuiensis* (Figure 1). Furthermore, the three specimens from Dupangling were grouped together with a small genetic variation to each other (< 0.001) and reciprocal monophyly to *H. zugii* with a moderate mtDNA sequence divergence (pairwise genetic distance ranged from 5.2%–5.8%, which were larger than the divergence level between *H. linnwayensis* and *H. ywanganensis* (3.6%)) (Table S2). Combined with the morphological characteristics of these specimens from Dupangling (see below), our molecular genetic results show that they deserve recognition as a new species of *Hemiphyllodactylus*.

Taxonomic account.

Hemiphyllodactylus dupanglingensis **sp. nov.** Zhang, Qian and Yang

Holotype. CSUFT 00402, adult male collected by Benjun WANG on 10 August 2018 in Hunan Dupangling National Nature Reserve (25°34'23.23" N, 111°23'21" E; 437 m a.s.l.) (Figure 2).

Paratypes. CSUFT 00403, 00404, 00405, three adult males, were collected by Benjun WANG from August to September 2018 in Hunan Dupangling National Nature Reserve (25°34'23.23" N, 111°23'21" E; 437 m a.s.l.). CSUFT 00401, one adult female, and CSUFT 00406, one adult male, were collected by Bing ZHANG and Jifu ZHOU on August 21, 2019, in Hunan Dupangling National Nature Reserve (25°34'23.23" N, 111°23'21" E; 437 m a.s.l.) (Figure 3).

Diagnosis. *Hemiphyllodactylus dupanglingensis* **sp. nov.** can be distinguished from all its congeners by a combination of following characters: (1) bisexual, presence of both males and females; (2) medium body size (SVL 39.4–44.7 mm in adult males, 40.8 mm in one adult female); (3) 9–11 chin scales; (4) postmental scales enlarged; (5) 3–4 circumnasal scales; (6) 2–3 scales between internasals; (7) 9–12 infralabials, 11–14 supralabials; (8) 14–16 dorsal scales and 10–11 ventral scales longitudinally arranged at midbody contained with one eye diameter; (9) a manual lamellar formula of 4-5-5-4 ($n = 1$) or 4-4-5-4 ($n = 4$), a pedal lamellar formula of 4-5-5-5 ($n = 4$) or 5-6-6-4 ($n = 1$); (10) four or five subdigital lamellae on first finger and first toe; (11) 21–25 continuous precloacal and femoral pores in males; (12) cloacal spurs 1–2; (13) no enlarged subcaudal scales; (14) dark transverse blotches on dorsal; (15) dark postorbital stripe present; (16) a linear series of white spots present on flank; (17) postsacral marking lack anterior projecting arms; and (18) pigmented gonadal tracts and caecum.

Description of holotype. Adult male, body slender, SVL 41.0 mm; tail regenerated, 29.3 mm in length; trunk length 19.4 mm (TrunkL/SVL 0.47); head longer than wide (HeadL 11.2 mm, HeadW 7.5, HeadW/HeadL 0.67), head 4.5 mm in depth (HeadD); eye diameter 2.6 mm (EyeD/HeadL 0.23), snout-eye length (SnEye) 4.7 mm; internarial distance (SnW) 1.5 mm.

Snout robust; rostral with a suture on upper edge, visible from above; 12/11 supralabials, enlarged from rostral to below eye; 9/9 infralabials; 3/3 circumnasal scales; two scales between supranasals; dorsal scales in one EyeD 15; ventral scales in one EyeD 11; a manual lamellar formula of 4–4–5–4, a pedal lamellar formula of 4–5–5–5; four lamellar on the first finger and four on the first toe; precloacal a femoral pore series continuous, 24 in number.

Coloration in life. We describe the coloration in life using a series of photos of paratype (CSUFT 401, adult female: Figure 4). Lateral view of head, presence of a white line beginning at loreal region through orbital to the back of the head, which gets thinner at neck and extends to dorsolateral. Two lines separated by some black-centered yellow pigments in the middle of the head front. Two dark postorbital lines present at edge of the white line. Iris copper red with brown reticulations, and pupil vertical with four black spots linked by black lines.

Dorsal color light yellow with dark reticulation transverse stripes starting behind the head and ending at postsacral marking; postsacral marking pale buff, chevron shaped; a series of light spots present on both sides on dorsolateral; fingers and toes are light yellow with black pigmentation on dorsal.

Ventral view of body and limbs pinkish white with light yellow edge ventral scales, and dense black dots present on each scale; gonadal tracts and caecum pigmented. Ventral view of tail orange.

Coloration in alcohol. Dorsal surface of head, body, and limbs greyish-brown, light orange postsacral mark faded to white. Ventral surface greyish-white, pigmented gonadal tracts, and caecum, light yellow edge on scales faded.

Variation. Measurements are shown in Table 1. Specimens vary in scale counts, subdigital lamellar, number of precloacal and femoral pores and body size. All recognized specimens share the same 2-5FingLm 4-4-5-4 except CSUFT 00401 (4-5-5-4). All recognized specimens share the same 2-5ToeLm 4-5-5-5 except CSUFT 00404 (5-6-6-4). Specimen CSUFT 00403 shows

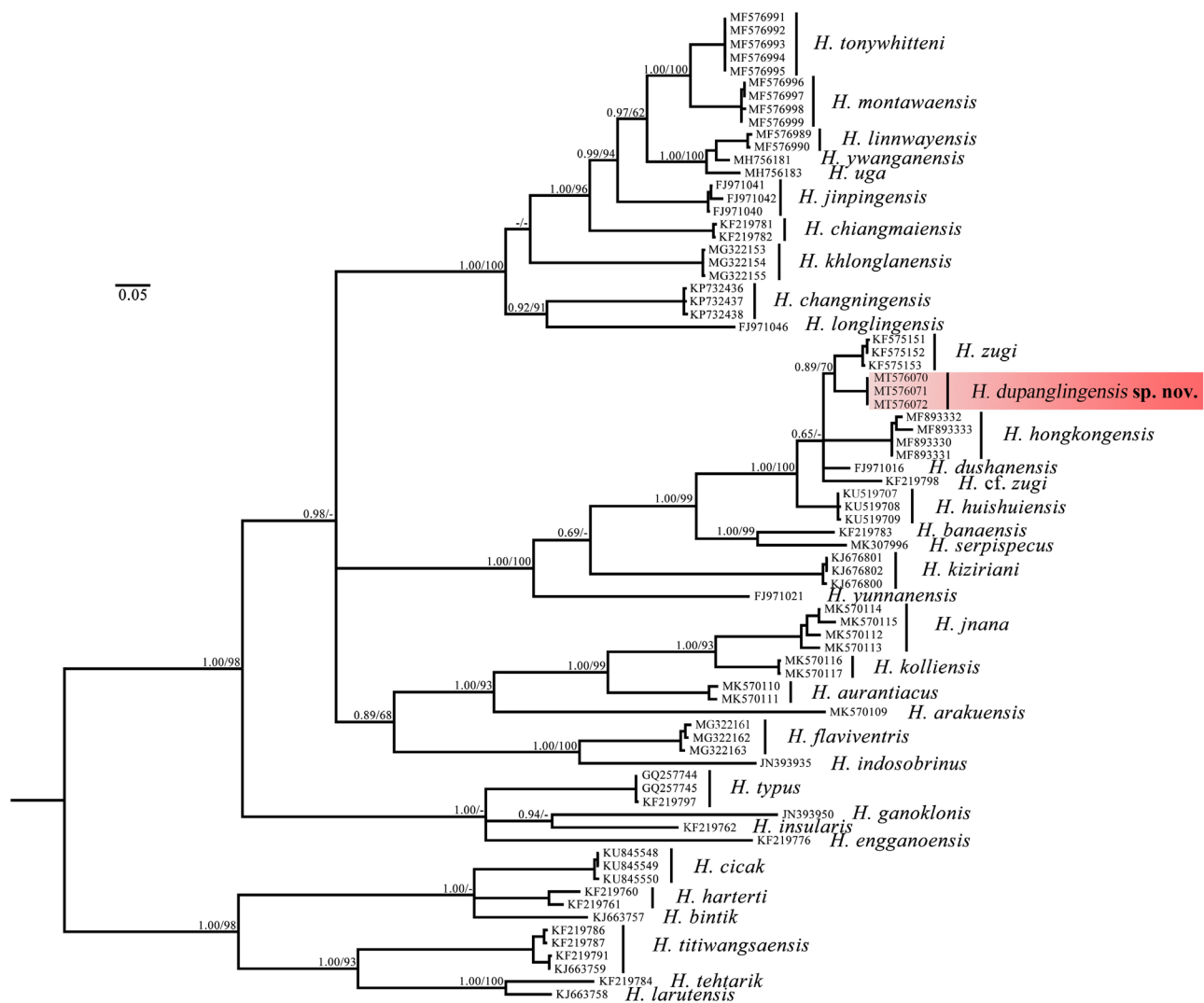


Figure 1 Bayesian inference tree of *Hemiphyllodactylus* species based on partial DNA sequences of the mitochondrial ND2 gene. Outgroups are not shown. Numbers before slashes indicate Bayesian posterior probabilities (> 0.6 retained) and numbers after slashes are bootstrap support for maximum likelihood (1000 replicates) analyses (> 60 retained). The symbol “-” represents the bootstrap value below 0.60/60%.

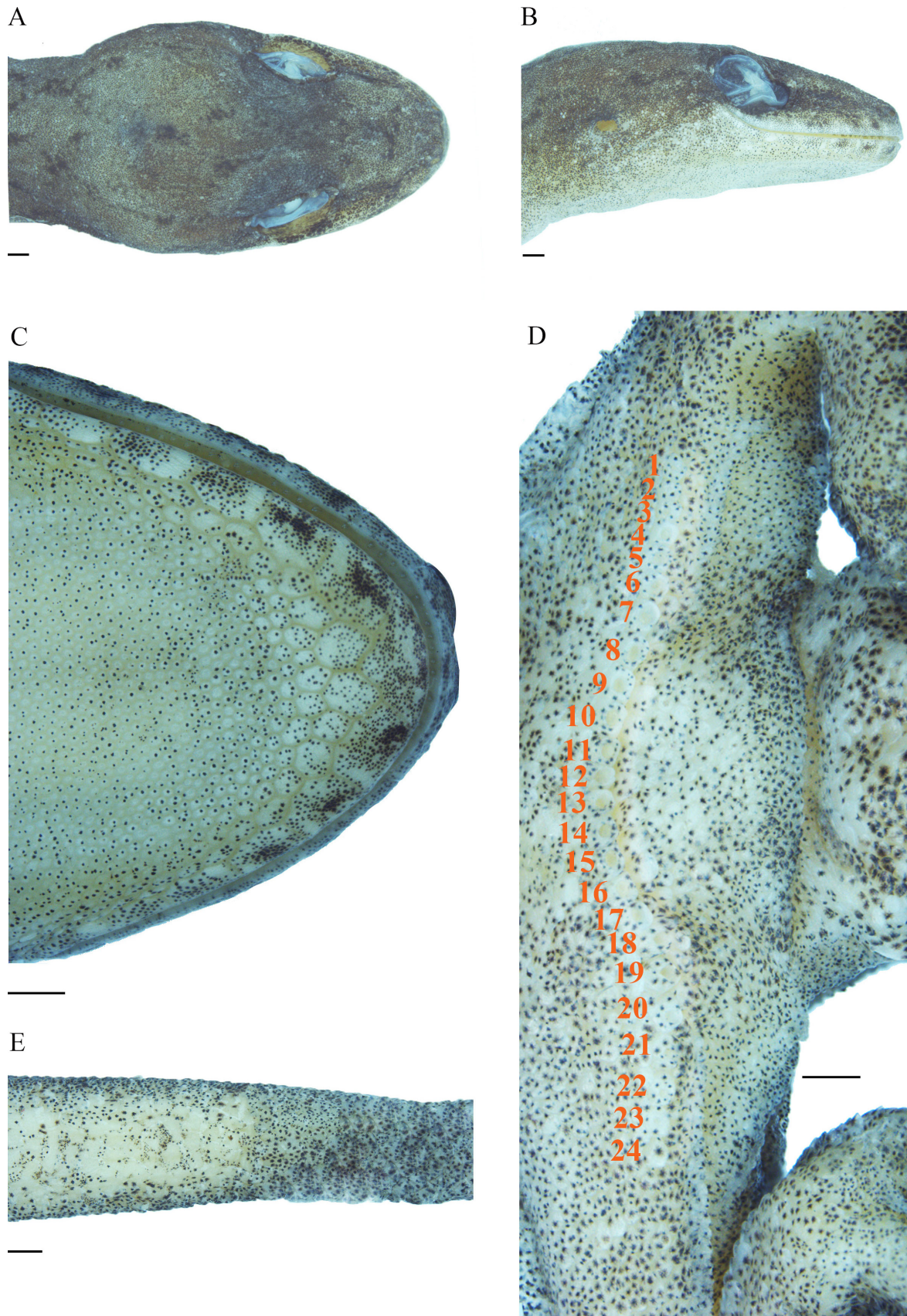


Figure 2 Holotype of *Hemiphyllodactylus dupanglingensis* sp. nov. in alcohol. A: dorsal view of head; B: lateral view of head; C: ventral view of head; D: ventral view of pubis and hind limbs showing pore series; E: ventral view of tail in middle part. Scale bars equal 0.5 mm.

a different dorsal color pattern. Instead of dark transverse bars, light paler irregular veins distributed on the dorsal of the head and body. Darker coloration on flanks extends from under-eye area to anterior portion of forefoot, with small white dots on flanks.

Comparisons. We show the diagnostic characters separating *H. dupanglingensis* **sp. nov.** with all named species of *Hemiphyllodactylus* (Table S3). We compared this species with eight closely related species (*H. banaensis*, *H. dushanensis*, *H. hongkongensis*, *H. huishuiensis*, *H. kiziriani*, *H. serpispecus*, *H. yunnanensis*, and *H. zugi*) (Table 2). *Hemiphyllodactylus dupanglingensis* **sp. nov.** can be differentiated from its eight closely related species by a combination of the following characters: maximum SVL 44.7 mm (vs. > 50 mm in *H. dushanensis*, *H. huishuiensis*, and *H. banaensis*); chin scales 9–11 (vs. < 9 in *H. hongkongensis*); internasal scales two or three (vs. 4–11 in *H. banaensis*); dorsal scales 14–16 (vs. > 16 in *H. banaensis*, *H. kiziriani*, *H. serpispecus*, and *H. zugi*); ventral scales 10 or 11 (vs. > 11 in *H. zugi* and < 10 in *H. dushanensis*, and *H. huishuiensis*); total lamellae on hand 17 or 18 (vs. < 17 in *H. hongkongensis*, *H. kiziriani*, *H. serpispecus*, *H. yunnanensis*, and *H. zugi*); total lamellae on foot 19–21 (vs. < 19 in *H. hongkongensis*, *H. kiziriani*, *H. serpispecus*, and *H. yunnanensis*); subdigital lamellae on the first finger four or five (vs. < 4 in *H. huishuiensis*); subdigital lamellae on the first toe four or five (vs. < 4 in *H. huishuiensis*); and continuous precloacal and femoral pores 21–25 (vs. < 21 in *H. huishuiensis*).

Etymology. The scientific name “*dupanglingensis*” is derived from its type locality Dupangling in Hunan province. As a common name we suggest Dupangling Slender Gecko in English and “Du Pang Ling Ban Ye Zhi Hu (都庞岭半叶趾虎)” in Chinese.

Distribution and natural history. The new species is currently known only from its type locality, Kongshuyan from Dupangling Nature Reserve, Hunan Province, China (Figure 5). This new species is nocturnal. In the daytime, individuals hide under wall seams, tile eaves, cupboards, and other concealed places, and vacate these at night to forage. All the individuals were found on the walls of human houses— that were surrounded by evergreen broad-leaf forests.

4. Discussion

The recognition of *H. dupanglingensis* **sp. nov.** increases the number of described species of *Hemiphyllodactylus* in China to eight, along with *H. changningensis*, *H. dushanensis*, *H. hongkongensis*, *H. huishuiensis*, *H. jinpingensis*, *H. longlingensis*, and *H. yunnanensis* (Grismer et al., 2013; Guo et al., 2015; Yan et al., 2016; Sung et al., 2018). These highlight the diversification of *Hemiphyllodactylus* species within China. *H. dushanensis*, *H. hongkongensis*, and *H. huishuiensis* in China *Hemiphyllodactylus* are close to *Hemiphyllodactylus dupanglingensis* **sp. nov.** in geographical range. The type locality of *H. dushanensis* is about 380

Table 2 Diagnostic characters (bold) separating *Hemiphyllodactylus dupanglingensis* **sp. nov.** from closely related species of *Hemiphyllodactylus*.

	<i>H. dupanglingensis</i> sp. nov.	<i>H. banaensis</i>	<i>H. dushanensis</i>	<i>H. hongkongensis</i>	<i>H. huishuiensis</i>	<i>H. kiziriani</i>	<i>H. serpispecus</i>	<i>H. yunnanensis</i>	<i>H. zugi</i>
Max SVL (mm)	44.7	51.0	50.6	43.0	51.2	40.8	41.9	49.3	46.6
Chin	9–11	7–10	8–10	5–6	8–10	6–9	7	6–11	9–12
Postmentals distinctly enlarged (1) or not (0)	1	1	1	1	1	1	1	1	1
CircNa	3 or 4	3	3 or 4	3 or 4	3	4	3	2–4	2 or 3
SnS	2 or 3	4–11	2 or 3	3 or 4	2 or 3	2 or 3	2	2–5	3–5
Suplab	11–14	9–12	11–13	10–12	9–11	10 or 11	11	8–13	10–13
Inflab	9–12	9–11	10–11	9–11	9–11	9–11	9	8–12	10–12
Dorsal	14–16	18–20	14–15	12–15	13–15	18–27	26	9–18	19–22
Ventral	10 or 11	9–12	8–9	9–10	7–9	11–15	10	6–12	14–16
2–5FingLm	4–4–5–4 4–5–5–4	3–4–4–4 4–5–5–4	3–4–5–4 4–5–5–4	3–3–4–4 3–4–4–4	3–4–4–4 4–5–5–4	3–4–4–4	3–4–4–4	3–3–3–3	3–4–4–4
2–5ToeLm	4–5–5–5 5–6–6–4	4–5–5–5	4–5–5–5 5–6–6–5	3–4–4–4 4–5–5–4	4–4–5–4 4–5–5–5	4–4–4–4 4–5–5–4	3–4–4–5	3–4–4–4	4–5–5–5
1FingLm	4 or 5	5	4 or 5	3–5	3	5	4	4–6	4 or 5
1ToeLm	4 or 5	4 or 5	5 or 6	5	3	5	4	4–7	4 or 5
Pore	21–25	15–21	24–26	24–25	0–20	8–13	11	11–25	18–21
Precloacal and femoral pore series separate (1) or continuous (0)	0	0	0	0	0	0	0	0	0
CloacS	1 or 2	1	1	1	1	1 or 2	2	0–2	1

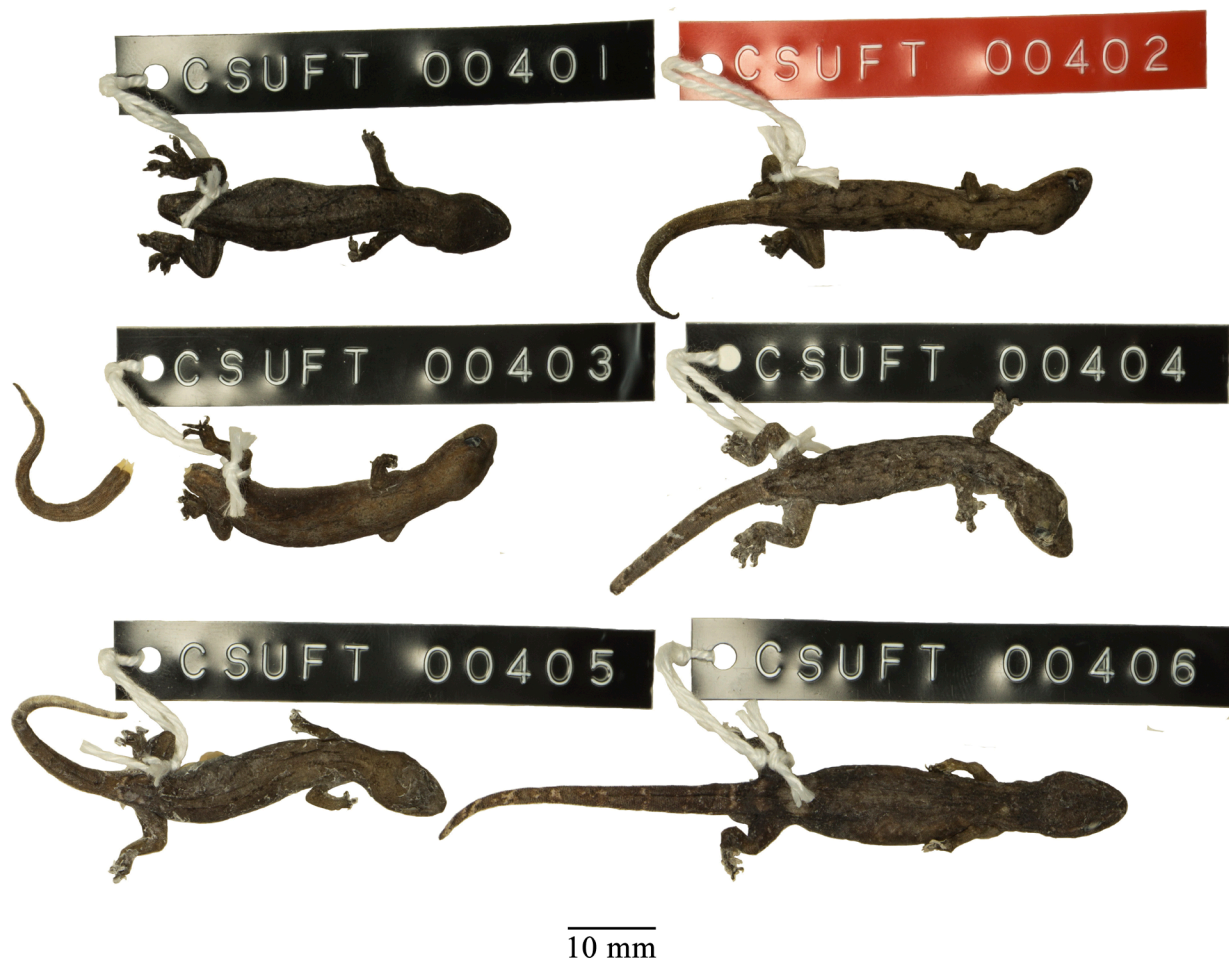


Figure 3 Type series of *Hemiphyllodactylus dupanglingensis* **sp. nov.** from specimens preserved in alcohol.

km west of the collection locality of *H. dupanglingensis* **sp. nov.** (Zhou *et al.*, 1981). The average mitochondrial ND2 sequence difference between *H. dupanglingensis* **sp. nov.** and *H. dushanensis* is 5.3%. The type locality of *H. huishuiensis* is about 470 km west of the collection locality of *H. dupanglingensis* **sp. nov.** (Yan *et al.*, 2016). The average mitochondrial ND2 sequence difference between *H. dupanglingensis* **sp. nov.** and *H. huishuiensis* is 7.8%. The type localities of *H. dushanensis* and *H. huishuiensis* are all located in the Miaoling mountains. The type locality of *H. hongkongensis* is Aberdeen Country Park, Hong Kong, about 470 km southeast of the collection locality of *H. dupanglingensis* **sp. nov.** (Sung *et al.*, 2018). The average mitochondrial ND2 sequence difference between *H. dupanglingensis* **sp. nov.** and *H. hongkongensis* is 9.8%. *Hemiphyllodactylus* specimens with an uncorrected mitochondrial ND2 sequence divergence value of $\geq 5\%$ were suspected to be different species (Grismer *et al.*, 2013). Consistent with Grismer *et al.* (2013), the ND2 sequence differences between *H. dupanglingensis* **sp. nov.**

and *H. dushanensis*, *H. hongkongensis*, or *H. huishuiensis* all exceed 5%. The collection locality of *H. dupanglingensis* **sp. nov.** and the type localities of the three species are separated by much warmer and drier low elevation habitats or other mountains. The discovery of *H. dupanglingensis* **sp. nov.** expands the distribution area of China *Hemiphyllodactylus* eastward to the Nanling mountains. The orogeny of this region and the common habits of the restricted, montane distribution of most *Hemiphyllodactylus* species may be the major driver for the formation of *H. dupanglingensis* **sp. nov.**

Most species of this genus are geographically restricted to highlands and island habitats (Grismer *et al.*, 2013). In China, only *H. hongkongensis* lives in a lower island habitat (Sung *et al.*, 2018). Other *Hemiphyllodactylus* species are all restricted to high elevation habitats (> 900 m) (Zhou *et al.*, 1981; Guo *et al.*, 2015; Yan *et al.*, 2016), which represent mid- to high-elevation taxa. However, the type locality of *H. dupanglingensis* **sp. nov.** is about 430 m. Dupangling is located in the middle part of Nanling

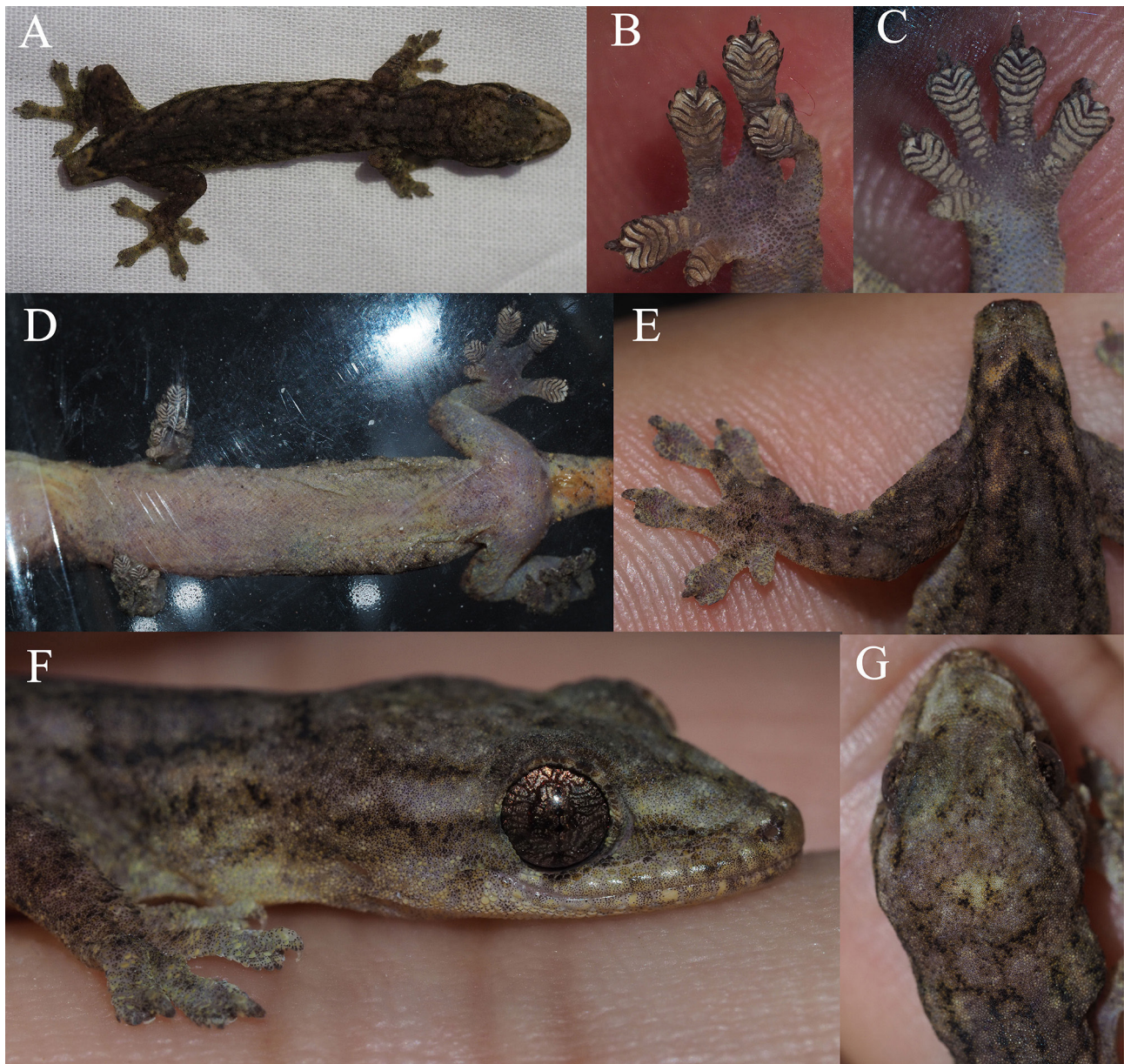


Figure 4 Living specimen (CSUFT 00401) of *Hemiphyllodactylus dupanglingensis* **sp. nov.** A: dorsal view; B: plantar view of left foot; C: volar view of right hand; D: ventral view; E: dorsal view of tail base; F: lateral view of head; G: dorsal view of head.

mountains. This unique geographical location contains large expanses of limestone karst forest. It is the most typical and representative transition zone from the middle subtropical zone to the south subtropical area in China, which contains high reptile diversity. The karst landforms of Dupangling produce rock substrates with a variety of microhabitats under the forest canopy. These provide effective thermoregulation, a stable microclimate, low illumination, and foraging opportunities for geckos and other reptiles (Grismer *et al.*, 2017). Many geckos are restricted to karst forest areas (Zug, 2010; Grismer *et al.*, 2013; Grismer *et al.*, 2017; Grismer *et al.*, 2018; Agarwal *et*

al., 2019; Eliades *et al.*, 2019). We have only collected this species of gecko in Kongshuyan of Dupangling, and we urge additional searches in the Nanling mountains for other “cryptic species.”

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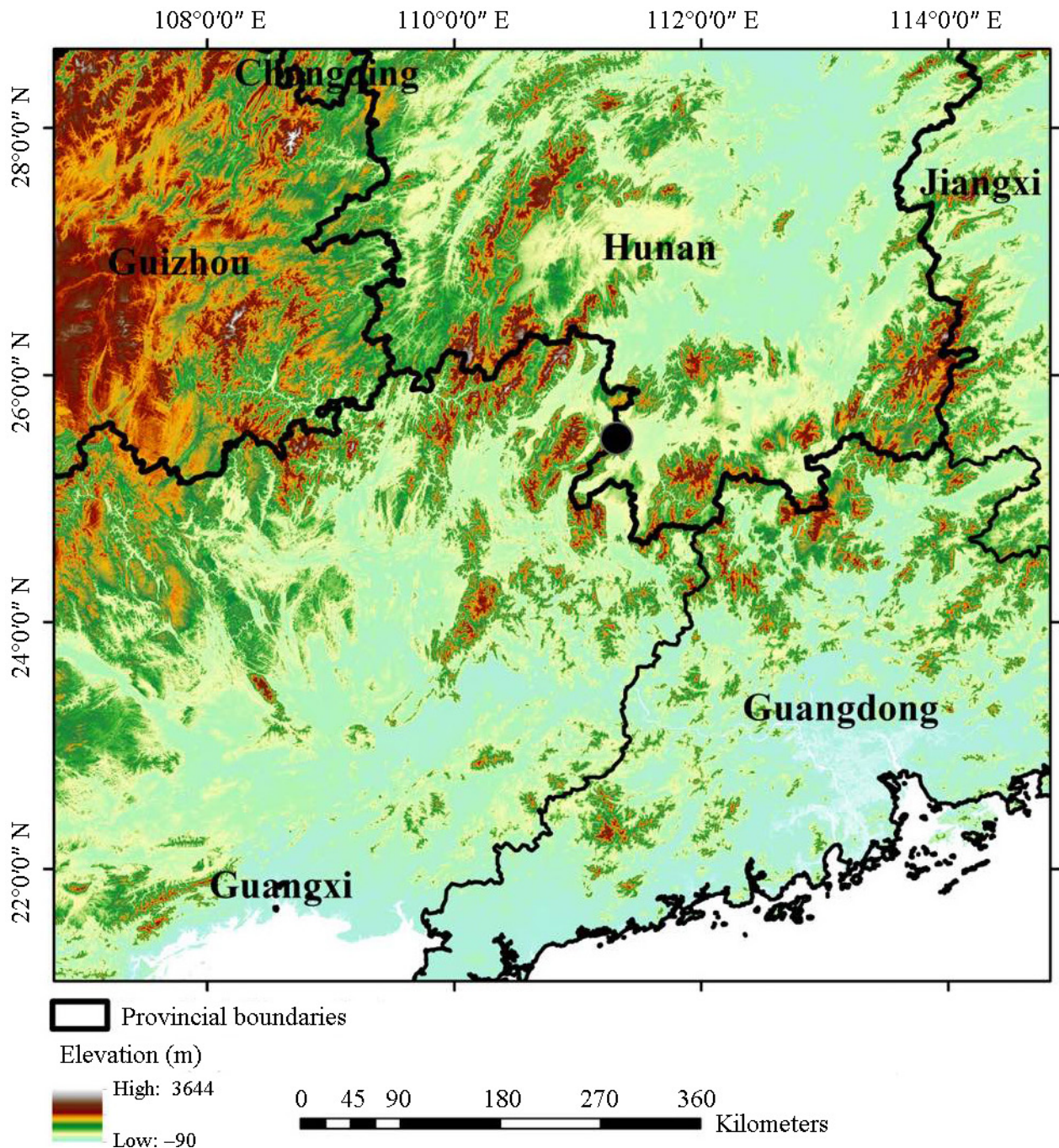


Figure 5 Map showing the collecting location of *Hemiphyllodactylus dupanglingensis* sp. nov. from Hunan Dupangling National Nature Reserve, China, which is indicated by the black dot.

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Appendix

Table S1 GenBank accession numbers, localities, and voucher information for all specimens used in this study.

ID	Species	GenBank No.	Locality	Voucher
1	<i>H. dupanglingensis</i> sp. nov.	MT576070	Dupangling, Dao County, Hunan, China	CSUFT 00401
2	<i>H. dupanglingensis</i> sp. nov.	MT576071	Dupangling, Dao County, Hunan, China	CSUFT 00405
3	<i>H. dupanglingensis</i> sp. nov.	MT576072	Dupangling, Dao County, Hunan, China	CSUFT 00406
4	<i>H. arakuensis</i>	MK570109	Araku, Visakhapatnam District, Andhra Pradesh, India	CES G068 (BNHS 2275)
5	<i>H. aurantiacus</i>	MK570111	Yercaud, Salem District, Tamil Nadu, India	AMB (no number)
6	<i>H. aurantiacus</i>	MK570110	Yercaud, Salem District, Tamil Nadu, India	AK 237
7	<i>H. banaensis</i>	KF219783	Ba Na-Nui Chua, Vietnam	TBCZ2450
8	<i>H. bintik</i>	KJ663757	Gunung Tebu, Terengganu, Malaysia	LSUHC 11216
9	<i>H. cf. zugi</i>	KF219798	Vinh Phu, Vietnam	MVZ 226500
10	<i>H. changningensis</i>	KP732436	Changning, Yunnan, China	NJNUh 00315
11	<i>H. changningensis</i>	KP732437	Changning, Yunnan, China	NJNUh 00325
12	<i>H. changningensis</i>	KP732438	Changning, Yunnan, China	NJNUh 00326
13	<i>H. chiangmaiensis</i>	KF219781	Chang Mai, Thailand	LSUHC 9503
14	<i>H. chiangmaiensis</i>	KF219782	Chang Mai, Thailand	LSUHC 9504
15	<i>H. cicak</i>	KU845548	Penang Hill, Penang, Malaysia	LSUHC 11762
16	<i>H. cicak</i>	KU845549	Penang Hill, Penang, Malaysia	LSUHC 11763
17	<i>H. cicak</i>	KU845550	Penang Hill, Penang, Malaysia	LSUHC 11764
18	<i>H. dushanensis</i>	FJ971016	Dushan, Guizhou, China	NJNUh00001
19	<i>H. engganoensis</i>	KF219776	Pulau Enggano, Sumatra, Indonesia	MVZ 239346
20	<i>H. flaviventris</i>	MG322161	Chanthaburi, Thailand	ZMKU TM001204N-09N 46CTI
21	<i>H. flaviventris</i>	MG322162	Chanthaburi, Thailand	ZMKU TM001204N-09N 47CTI
22	<i>H. flaviventris</i>	MG322163	Chanthaburi, Thailand	ZMKU TM001204N-09N 48CTI
23	<i>H. ganoklonis</i>	JN393950	Ngercheu, Palau	USNM 563671
24	<i>H. harterti</i>	KF219761	Bukit Larut, Malaysia	LSUHC 10383
25	<i>H. harterti</i>	KF219760	Bukit Larut, Malaysia	LSUHC 10384
26	<i>H. hongkongensis</i>	MF893330	Aberdeen Country Park, Hong Kong, China	SYS r001735
27	<i>H. hongkongensis</i>	MF893331	Aberdeen Country Park, Hong Kong, China	SYS r001728
28	<i>H. hongkongensis</i>	MF893332	Aberdeen Country Park, Hong Kong, China	SYS r001729
29	<i>H. hongkongensis</i>	MF893333	Aberdeen Country Park, Hong Kong, China	SYS r001730
30	<i>H. huishuiensis</i>	KU519707	Huishui, Guizhou, China	NJNUh00729-739
31	<i>H. huishuiensis</i>	KU519708	Huishui, Guizhou, China	NJNUh00729-746
32	<i>H. huishuiensis</i>	KU519709	Huishui, Guizhou, China	NJNUh00851
33	<i>H. indosobrinus</i>	JN393935	Champasak, Pakxong, Laos	FMNH 258695
34	<i>H. insularis</i>	KF219762	Mindanao, Philippines	KU 314962
35	<i>H. jinningensis</i>	FJ971040	Jinping, Yunnan, China	n/a
36	<i>H. jinningensis</i>	FJ971041	Jinping, Yunnan, China	NJNUh00138
37	<i>H. jinningensis</i>	FJ971042	Jinping, Yunnan, China	n/a
38	<i>H. jnana</i>	MK570112	NCBS, Bangalore Urban District, Karnataka, India	CES G174
39	<i>H. jnana</i>	MK570113	Aiyur, Hosur District, Tamil Nadu, India	CES G173
40	<i>H. jnana</i>	MK570114	Yelagiri, Vellore District, Tamil Nadu, India	CYL01
41	<i>H. jnana</i>	MK570115	Kolar, Kolar District, Karnataka, India	CES G470
42	<i>H. khlonglanensis</i>	MG322153	Kamphaeng Phet, Thailand	ZMKU TM000999N
43	<i>H. khlonglanensis</i>	MG322154	Kamphaeng Phet, Thailand	ZMKU TM001000N
44	<i>H. khlonglanensis</i>	MG322155	Kamphaeng Phet, Thailand	ZMKU TM001001N
45	<i>H. kiziriani</i>	KJ676800	Luang Prabang, Laos	IEBR A.2014.3
46	<i>H. kiziriani</i>	KJ676801	Luang Prabang, Laos	IEBR A.2014.4
47	<i>H. kiziriani</i>	KJ676802	Luang Prabang, Laos	IEBR A.2014.5
48	<i>H. kolliensis</i>	MK570117	Kolli Hills, Namakkal District, Tamil Nadu, India	AK 276

(Continued Table S1)

ID	Species	GenBank No.	Locality	Voucher
49	<i>H. kolliensis</i>	MK570116	Kolli Hills, Namakkal District, Tamil Nadu, India	CES G138
50	<i>H. larutensis</i>	KJ663758	Bukit Larut, Malaysia	LSUHC 11295
51	<i>H. linnwayensis</i>	MF576989	Taunggyi District, Shan State, Myanmar	LSUHC 12969
52	<i>H. linnwayensis</i>	MF576990	Taunggyi District, Shan State, Myanmar	LSUHC 12987
53	<i>H. longlingensis</i>	FJ971046	Yunnan, China	NJNUh00104
54	<i>H. montawaensis</i>	MF576996	Taunggyi District, Shan State, Myanmar	LSUHC 10310
55	<i>H. montawaensis</i>	MF576997	Taunggyi District, Shan State, Myanmar	LSUHC 10311
56	<i>H. montawaensis</i>	MF576998	Taunggyi District, Shan State, Myanmar	LSUHC 10312
57	<i>H. montawaensis</i>	MF576999	Taunggyi District, Shan State, Myanmar	LSUHC 10313
58	<i>H. serpispecus</i>	MK307996	Houaphanh Province, Laos	NUOL 00476
59	<i>H. tehtarik</i>	KF219784	Gunung Tebu, Terengganu, Malaysia	LSUHC 10904
60	<i>H. titiwangsaensis</i>	KF219786	Cameron Highlands, Malaysia	LSUHC 10713
61	<i>H. titiwangsaensis</i>	KF219787	Cameron Highlands, Malaysia	LSUHC 10714
62	<i>H. titiwangsaensis</i>	KF219791	Cameron Highlands, Malaysia	LSUHC 7208
63	<i>H. titiwangsaensis</i>	KJ663759	Cameron Highlands, Pahang, Malaysia	JAM 1970
64	<i>H. tonywhitteni</i>	MF576991	Taunggyi District, Shan State, Myanmar	LSUHC 13026
65	<i>H. tonywhitteni</i>	MF576992	Taunggyi District, Shan State, Myanmar	LSUHC 13027
66	<i>H. tonywhitteni</i>	MF576993	Taunggyi District, Shan State, Myanmar	LSUHC 13028
67	<i>H. tonywhitteni</i>	MF576994	Taunggyi District, Shan State, Myanmar	LSUHC 13029
68	<i>H. tonywhitteni</i>	MF576995	Taunggyi District, Shan State, Myanmar	LSUHC 13020
69	<i>H. typus</i>	GQ257744	Papua New Guinea	ABTC 49760
70	<i>H. typus</i>	GQ257745	Suva, Fiji	ABTC 32736
71	<i>H. typus</i>	KF219797	Tasik Chini, Malaysia	LSUHC 8751
72	<i>H. uga</i>	MH756183	Mandalay Region, Myanmar	USNM 570733
73	<i>H. yunnanensis</i>	FJ971021	Kunming, Yunnan, China	NJNUh00056
74	<i>H. ywanganensis</i>	MH756181	Taunggyi District, Shan State, Myanmar	LSUHC 13138
75	<i>H. zugi</i>	KF575151	Ha Lang, Cao Bang, Vietnam	IEBRA.2013.20
76	<i>H. zugi</i>	KF575152	Ha Lang, Cao Bang, Vietnam	IEBRA.2013.21
77	<i>H. zugi</i>	KF575153	Ha Lang, Cao Bang, Vietnam	ZFMK 94782
78	<i>Cyrtodactylus lorae</i>	EU268350	Milne Bay, Bunis, Papua New Guinea	FK 7709
79	<i>Gehyra fehlmanni</i>	JN393948	Imported from Malaysia	TG 00723
80	<i>Gehyra insulensis</i>	GQ257784	Krakatau, Indonesia	ABTC 13940
81	<i>Gehyra mutilata</i>	JN393914	Pursat Province, Phnom Aural, Cambodia	LSUHC 7379
82	<i>Gekko gekko</i>	AF114249	Phuket Island, Thailand	MVZ 215314
83	<i>Lepidodactylus lugubris</i>	JN393944	Singapore	ZRC 24847

Table S3 Diagnostic characters separating the species from other nominal taxa of *Hemiphyllodactylus*.

Species	Max SVL (mm)	Chin	Postmentals distinctly enlarged (1) or not (0)	CircNa	SnS	Suplab	Inflab	Dorsal	Ventral	2-5FingLm	2-5ToeLm	IFingLm	IToeLm	Pore	Predorsal and femoral pore series separate (1) or continuous (0)	CloacS
<i>daopingensis</i> sp. nov.	44.7	9-11	1	3 or 4	2 or 3	11-14	9-12	14-16	10 or 11	4-4-5-4/4-5-5-4	4-5-5-5/5-6-6-4	4 or 5	4 or 5	21-25	0	1 or 2
<i>aurantiacus</i>	37.9	10-14	0	2-4	3-6	10-13	8-12	11-17	8-12	2-2-2-2	2-2-3-2/2-2-3-3	3 or 4	4 or 5	16-25	1	1-3
<i>arakuensis</i>	39.0	8-11	0	2	2-3	9-12	9-12	13-16	7-9	2-2-2-2	2-3-3-3/3-3-3-3	4 or 5	5 or 6	\	\	2
<i>banensis</i>	51.0	7-10	1	3	4-11	9-12	9-11	18-20	9-12	3-4-4-4/4-5-5-4	4-5-5-5	5	4 or 5	15-21	0	1
<i>binik</i>	36.6	7	1	5	3	11	12	17	7	2-4-4-3	3-4-4-4	4	5	\	\	1
<i>changningensis</i>	43.8	7 or 8	1	3 or 4	2 or 3	8-11	8-10	11-15	6-8	3-3-3-3/3-4-4-3	3-3-3-3/3-4-4-4	3 or 4	3 or 4	19-22	0	1 or 2
<i>chiangnaiensis</i>	41.2	8-12	1	3 or 4	1-3	9-11	9-12	11-21	6-10	3-3-3-3/3-3-4-3	3-3-3-3/3-4-3-3	3 or 4	3 or 4	17-25	0	1
<i>cicak</i>	31.4	7	1	3	1-2	8	8	16-18	10 or 11	2-3-3-2	2-3-3-3	2	2	42	0	2
<i>dahanensis</i>	50.6	8-10	1	3 or 4	2 or 3	11-13	10-11	14-15	8-9	3-4-5-4/4-5-5-4	4-5-5-5/5-6-6-5	4 or 5	5 or 6	24-26	0	1
<i>engganensis</i>	37.3	6	0	5	3 or 4	12	12	24 or 25	14	4-5-5-4/4-4-5-4	4-5-5-5	4 or 5	4 or 5	42	0	5
<i>flaviventris</i>	39.2	7-10	\	5	1-5	9-12	8-11	16-18	8-10	4-4-4-4	4-5-5-5	5	5	9	\	1 or 2
<i>gonokomis</i>	34.2	9-12	0	2-4	3-5	8-11	8-10	11-18	9-12	3-4-4-3	3-4-4-4	3-5	3-5	16-28	1	1-4
<i>hartii</i>	39.0	6-8	1	2-5	3 or 4	10 or 11	10 or 11	14-19	6-14	3-3-3-3	3-4-4-3	3	4	42-45	0	1 or 2
<i>hongkongensis</i>	43.0	5-6	1	3 or 4	3 or 4	10-12	9-11	12-15	9-10	3-3-4-4/3-4-4-4	3-4-4-4/4-5-5-4	3-5	3	24-25	0	1
<i>huishuensis</i>	51.2	8-10	1	3	2 or 3	9-11	9-11	13-15	7-9	3-4-4-4/4-5-5-4	4-4-5-4/4-5-5-5	3	3	0-20	0	1
<i>indosibiricus</i>	39.8	8	1	3	3	15	12	30	11	4-5-5-4	4-5-5-5	4	5	18	0	1
<i>insularis</i>	37.3	8-14	0	1-4	2-4	9-13	9-11	13-18	8-14	3-3-3-3	3-4-4-4	2-5	3-6	17-38	1	0-3
<i>jirana</i>	41.0	10-12	0	2	3-5	10-12	9-13	16-20	11-15	2-2-2-2	2-2-2-2	4 or 5	4 or 5	\	\	2
<i>jipingensis</i>	39.6	7-9	1	3-4	2-3	9-11	9-11	11-12	5-7	3-4-4-4/4-4-4-4	4-4-4-4	4	4 or 5	20-24	0	1
<i>khlonglanensis</i>	43.1	7 or 8, 10	\	5	2-4	9-12	8-11	10-15	7-10	3-4-4-4/4-4-4-4	4-4-4-4	5 or 6	5	19 or 20	0	1
<i>kollensis</i>	39.0	10-12	0	2	3 or 4	9-11	10 or 11	16	10-13	2-2-2-2	2-2-2-2	3 or 4	4 or 5	\	\	2
<i>kiziliani</i>	40.8	6-9	1	4	2 or 3	10 or 11	9-11	18-27	11-15	3-4-4-4	4-4-4-4/4-5-5-4	5	5	8-13	0	1 or 2
<i>larutensis</i>	52.2	6-10	1	3-5	3	9 or 10	7-10	13-20	7-13	\	\	3 or 4	3-5	27-36	0	2 or 3
<i>limnayeensis</i>	41.5	4-6	1	5	2	9 or 10	8	13 or 14	8	4-4-4-4	4-5-4-4/4-5-5-4	3 or 4	4 or 5	\	\	1
<i>longlingensis</i>	45.7	7-9	1	4-5	1-3	9-10	8-10	10-14	6-7	3-4-4-4/3-4-4-4/3-4-4-4/4-4-5-4	4-4-4-4/4-5-5-4	4-5	4-6	16-27	0	1 or 2
<i>montanaensis</i>	40.1	4-7	1	4-6	1-4	8-10	8 or 9	13 or 14	7 or 8	3-3-3-3/3-4-4-3	3-4-4-4/4-5-5-5	3 or 4	3 or 4	19-21	0	1
<i>sepiusaeus</i>	41.9	7	1	3	2	11	9	26	10	3-4-4-4	3-4-4-5	4	4	11	0	2
<i>tehrak</i>	40.4	8	1	5 or 1	3	11	10	18	12	3-3-3-3	3-4-5-4	5	5	0	\	3
<i>titiwangensis</i> *	62.1	8 or 9	1	3	1-3	9-11	8-10	14-19	7-9	3-4-4-4	4-5-5-5	4-6	5-8	17-39	0	1-4
<i>tonywhitii</i>	38.3	5-8	1	3-5	2-4	8 or 9	8	13-16	7-9	4-4-4-4/4-5-5-4	3-4-4-4/4-5-5-5	3	3 or 4	20-26	0	1
<i>typus</i> *	46.1	9-14	1	1-5	1-5	9-14	7-13	12-19	8-14	3-4-4-4	4-4-5-4	4 or 5	5 or 6	0-26	1 or 0	1-5
<i>uga</i>	39.0	8-10	1	5	2 or 3	9 or 10	8-10	13-15	6-8	3-3-3-3/2-3-3-3/3-2-3-3	3-3-3-3	2 or 3	2 or 3	18-22	0	1
<i>yunnanensis</i> *	49.3	6-11	1	2-4	2-5	8-13	8-12	9-18	6-12	3-3-3-3	3-4-4-4	4-6	4-7	11-25	0	0-2
<i>yuwongensis</i>	38.0	10	1	5	2 or 3	9 or 10	10	13-15	7 or 8	3-3-3-3/3-3-4-3	3-3-3-3	3	2 or 3	26	0	1
<i>zugl</i>	46.6	9-12	1	2 or 3	3-5	10-13	10-12	19-22	14-16	3-4-4-4	4-5-5-5	4 or 5	4 or 5	18-21	0	1

Diagnostic and potentially diagnostic characters are set in bold; \ = data unavailable.

*Taxa containing multiple undescribed species, but encompassed within the taxonomy of Zug (2010).